

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/485,163

1812

DATE: 10/29/97
TIME: 15:37:02

INPUT SET: S21268.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Beaudry, Gary A.
Maddon, Paul J.

(ii) TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.24

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/485,163
(B) FILING DATE: 07-JUN-1995
(C) CLASSIFICATION:

(vii) ATTORNEY/AGENT INFORMATION:

(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US

(viii) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 278-0400
(B) TELEFAX: (212) 391-0525
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown

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47 (D) TOPOLOGY: unknown
48
49 (ii) MOLECULE TYPE: peptide
50
51 (vi) ORIGINAL SOURCE:
52 (A) ORGANISM: homo sapien
53 (G) CELL TYPE: lymphocyte
54
55
56
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59 Phe Glu Arg Lys Cys Cys Val Gln Cys Pro Pro Cys Asp
60 1 5 10
61

62 (2) INFORMATION FOR SEQ ID NO:2:
63
64 (i) SEQUENCE CHARACTERISTICS:
65 (A) LENGTH: 1796 base pairs
66 (B) TYPE: nucleic acid
67 (C) STRANDEDNESS: double
68 (D) TOPOLOGY: unknown
69
70 (ii) MOLECULE TYPE: cDNA
71
72 (vi) ORIGINAL SOURCE:
73 (A) ORGANISM: Homo sapiens
74 (G) CELL TYPE: Lymphocyte
75
76
77

78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
79
80 CAAGCCCAGA GCCCTGCCAT TTCTGTGGGC TCAGGTCCCT ACTGCTCAGC CCCTTCCTCC 60
81
82 CTCGGCAAGG CCACAATGAA CCGGGGAGTC CCTTTTAGGC ACTTGCTTCT GGTGCTGCAA 120
83
84 CTGGCGCTCC TCCCAGCAGC CACTCAGGGA AAGAAAGTGG TGCTGGGCAA AAAAGGGGAT 180
85
86 ACAGTGGAAC TGACCTGTAC AGCTTCCCAG AAGAAGAGCA TACAATTCCA CTGGAAAAAC 240
87
88 TCCAACCAGA TAAAGATTCT GGGAAATCAG GGCTCCTTCT TAACTAAAGG TCCATCCAAG 300
89
90 CTGAATGATC GCGCTGACTC AAGAAGAAGC CTTTGGGACC AAGGAAACTT CCCCCTGATC 360
91
92 ATCAAGAATC TTAAGATAGA AGACTCAGAT ACTTACATCT GTGAAGTGGA GGACCAGAAG 420
93
94 GAGGAGGTGC AATTGCTAGT GTTCGGATTG ACTGCCAACT CTGACACCCA CCTGCTTCAG 480
95
96 GGGCAGAGCC TGACCCTGAC CTTGGAGAGC CCCCCTGGTA GTAGCCCCTC AGTGCAATGT 540
97
98 AGGAGTCCAA GGGGTAAAAA CATACAGGGG GGAAGACCC TCTCCGTGTC TCAGCTGGAG 600
99

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100	CTCCAGGATA GTGGCACCTG GACATGCACT GTCTTGCAGA ACCAGAAGAA GGTGGAGTTC	660
101		
102	AAAATAGACA TCGTGGTGCT AGCTTTCGAG CGCAAATGTT GTGTGAGTG CCCACCGTGC	720
103		
104	CCAGGTAAGC CAGCCCAGGC CTCGCCCTCC AGCTCAAGGC GGGACAGGTG CCCTAGAGTA	780
105		
106	GCCTGCATCC AGGGACAGGC CCCAGCTGGG TGCTGACACG TCCACCTCCA TCTCTTCCTC	840
107		
108	AGCACCACT GTGGCAGGAC CGTCAGTCTT CCTCTTCCCC CAAAAACCCA AGGACACCTT	900
109		
110	CATGATCTCC CGGACCCCTG AGGTCACGTG CGTGGTGGTG GACGTGAGCC ACGAAGACCC	960
111		
112	CGAGGTCCAG TTCAACTGGT ACGTGGACGG CGTGGAGGTG CATAATGCCA AGACAAAGCC	1020
113		
114	ACGGGAGGAG CAGTTCAACA GCACGTTCCG TGTGGTCAGC GTCCCTCACCG TTGTGCACCA	1080
115		
116	GGACTGGCTG AACGGCAAGG AGTACAAGTG CAAGGTCTCC AACAAAGGCC TCCAGCCCC	1140
117		
118	CATCGAGAAA ACCATCTCCA AAACCAAAGG TGGGACCCGC GGGGTATGAG GGCCACATGG	1200
119		
120	ACAGAGGCCG GCTCGGCCCA CCCTCTGCCC TGGGAGTGAC CGCTGTGCCA ACCTCTGTCC	1260
121		
122	CTACAGGGCA GCCCCGAGAA CCACAGGTGT ACACCCTGCC CCCATCCCGG GAGGAGATGA	1320
123		
124	CCAAGAACCA GGTACGCCTG ACCTGCCTGG TCAAAGGCTT CTACCCCAGC GACATCGCCC	1380
125		
126	TGGAGTGGGA GAGCAATGGG CAGCCGGAGA ACAACTACAA GACCACACCT CCCATGCTGG	1440
127		
128	ACTCCGACGG CTCCTTCTTC CTCTACAGCA AGCTCACCGT GGACAAGAGC AGGTGGCAGC	1500
129		
130	AGGGGAACTG CTTCTCATGC TCCGTGATGC ATGAGGCTCT GCACAACCAC TACACGCAGA	1560
131		
132	AGAGCCTCTC CCTGTCTCCG GGTAAATGAG TGCCACGGCC GGCAAGCCCC CGCTCCCCAG	1620
133		
134	GCTCTCGGGG TCGCGTGAGG ATGCTTGGA CGTACCCCGT GTACATACTT CCCAGGCACC	1680
135		
136	CAGCATGGAA ATAAAGCACC CAGCGCTGCC CTGGGCCCCCT GCGAGACTGT GATGGTTCTT	1740
137		
138	TCCGTGGGTC AGGCCGAGTC TGAGGCCTGA GTGGCATGAG GGAGGCAGAG TGGGTC	1796
139		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homo sapien
- (G) CELL TYPE: lymphocyte

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153
154
155
156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
157
158 Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu
159 1 5 10 15
160
161
162 Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys
163 20 25 30
164
165
166 Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
167 35 40 45
168
169
170 Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
171 50 55 60
172
173
174 Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
175 65 70 75 80
176
177
178 Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
179 85 90 95
180
181
182
183 Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
184 100 105 110
185
186
187 Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
188 115 120 125
189
190
191 Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
192 130 135 140
193
194
195 Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
196 145 150 155 160
197
198 Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
199 165 170 175
200
201
202 Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
203 180 185 190
204
205

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206	Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Phe	Glu	Arg	Lys	Cys
207			195					200					205			
208																
209																
210	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser
211		210					215					220				
212																
213																
214	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
215	225					230					235					240
216																
217	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
218					245					250					255	
219																
220																
221	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
222				260					265					270		
223																
224																
225	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	Val
226			275					280					285			
227																
228																
229	Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
230		290					295					300				
231																
232																
233	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
234	305					310					315					320
235																
236	Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
237					325					330					335	
238																
239																
240	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
241				340					345					350		
242																
243																
244	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
245			355					360					365			
246																
247																
248	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp
249		370					375					380				
250																
251																
252	Ser	Asp	Gly													

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SEQUENCE VERIFICATION REPORT
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Original Text